



SEQUENCE LISTING

<110> Cahoon, Rebecca E.  
Miao, Gou-Hau  
Powell, Wayne

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<151> September 8, 1998

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<213> Zea mays

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 <213> Oryza sativa

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 Glu Lys Leu Gly Pro Asp Ile Ala Asn Lys Glu His Glu Phe Thr Arg  
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 165 170 175  
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 Ala Met Arg Asp Ser Glu Val Asp Tyr Thr Val Gly Ala Ile Leu Ala  
 210 215 220  
 Asn Pro Gln Asn Glu Ser Pro Trp Arg Tyr Leu Lys Gly Leu Tyr Lys  
 225 230 235 240  
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 245 250 255  
 Leu Lys Val Leu Lys His Asp Ser Thr Cys Val Phe Ala Leu Ser Leu  
 260 265 270  
 Leu Leu Asp Leu Leu Gln Ile Gly Leu Gln Pro Ser Asp Glu Leu Lys  
 275 280 285  
 Gly Thr Ile Glu Ala Ile Lys Asn Ser Asp Pro Glu Ala Asp Glu Ala  
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 Val Asp Ala Asp Leu Ala Thr Ala Ile Cys Ser Ile Leu Gln Arg Cys  
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<212> PRT  
<213> Glycine max

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35 40 45  
Glu Val Met Asp Tyr Phe Arg Ala Val Tyr Leu Thr Asp Glu Arg Ser  
50 55 60  
Pro Arg Ala Leu Ala Leu Thr Ala Glu Ala Val Gln Phe Asn Ser Gly  
65 70 75 80  
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85 90 95  
Val Asp Leu Asn Asp Glu Leu Asp Phe Val Glu Arg Met Ala Ala Gly  
100 105 110  
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115 120 125  
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180 185 190  
Arg Tyr Phe Val Ile Thr Arg Ser Pro Phe Leu Gly Gly Leu Lys Ala  
195 200 205  
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210 215 220  
Pro Glu Asn Glu Ser Ser Trp Arg Tyr Leu Arg Gly Leu Tyr Lys Gly  
225 230 235 240

Glu Thr Thr Ser Trp Val Asn Asp Pro Gln Val Ser Ser Val Cys Leu  
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Lys Ile Leu Arg Thr Lys Ser Asn Tyr Val Phe Ala Leu Ser Thr Ile  
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Leu Asp Leu Ile Cys Phe Gly Tyr Gln Pro Asn Glu Asp Ile Arg Asp  
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Ala Ile Asp Ala Leu Lys Thr Ala Asp Met Asp Lys Gln Asp Leu Asp  
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Asp Asp Glu Lys Gly Glu Gln Gln Asn Leu Asn Ile Ala Arg Asn Ile  
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 <212> PRT  
 <213> Glycine max

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Pro	Arg	Ala	Leu	Ala	Leu	Thr	Ala	Glu	Ala	Val	Gln	Phe	Asn	Ser	Gly
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<212> DNA  
<213> Triticum aestivum

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35 40 45  
Asp Ala Ile His Leu Asn Pro Gly Asn Tyr Thr Val Trp His Phe Arg  
50 55 60  
Arg Val Val Leu Glu Ala Leu Asp Ala Asp Leu Leu Leu Glu Met His  
65 70 75 80  
Phe Val Asp Gln Ile Ala Glu Ser Asn Pro Lys Asn Tyr Gln Val Trp  
85 90 95



His His Lys Arg Trp Leu Ala Glu Lys Ile Gly Pro Asp Ala Ala Asn  
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 Ser Glu His Asp Phe Thr Arg Lys Ile Leu Ala Met Asp Ala Lys Asn  
 115 120 125  
 Tyr His Ala Trp Ser His Arg Gln Trp Val Leu Gln Ala Leu Gly Gly  
 130 135 140  
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 Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr Leu Val Val Thr Arg Ser  
 165 170 175  
 Pro Ile Leu Gly Gly Leu Ala Ala Met Arg Asp Ser Glu Val Asp Tyr  
 180 185 190  
 Thr Val Glu Ala Ile Met Val Asn Pro Gln Asn Glu Ser Pro Trp Arg  
 195 200 205  
 Tyr Leu Arg Gly Leu Tyr Lys Asp Asp Asn Asn Leu Leu Val Ala Asp  
 210 215 220  
 Asn Arg Ile Ser Asp Ala Cys Leu Lys Val Leu Asn Lys Asp Trp Thr  
 225 230 235 240  
 Cys Val Phe Ala Leu Ser Phe Leu Leu Asp Leu Leu Arg Met Gly Leu  
 245 250 255  
 Gln Pro Ser Asn Glu Leu Lys Gly Thr Ile Glu Ala Met Glu Asn Ser  
 260 265 270  
 Asp Pro Glu Thr Gly His Ala Asp Ile Ala Val Ala Val Cys Ser Ile  
 275 280 285  
 Leu Gln Lys Cys Asp Pro Leu Arg Ile Asn Tyr Trp Ser Trp Tyr Gln  
 290 295 300  
 Thr Thr Leu Ser Ser  
 305

<210> 11  
 <211> 1359  
 <212> DNA  
 <213> Zea mays

<400> 11  
 atggaccct cccgcagtc gacgccgcc accggagacg acccggcagc ggcggcggat 60  
 cccgacctac cgaggctcac ggtgacgcag gtggagcaga tgaagggtga ggccaggggt 120  
 ggcgacatct accgctccct ctccggggcc gcgccaaca cgaaatccat catgctagag 180  
 ctgtggcgtg atcagcatat cgagtatctg acgcctgggc tgaggcatat gggaccagcc 240  
 tttcatgttc tagatgccaa tcgcccttgg ctatgctact ggatggttca tccacttgct 300  
 ttgctggatg aagcacttga tgatgatctt gagaatgata tcatagactt cttagctcga 360  
 tgtcaggata aagatgggtg atatagtggt ggacctggac agttgcctca cctagctacg 420  
 acttatgctg ctgtaaatac acttgtagca atagggagcg aaagagcatt gtcataatc 480  
 aataggggca acctgtacaa ttttatgctg cagatgaaag atgtatcagg tgctttcaga 540  
 atgcatgatg gtggcgaaat tgatgtccgt gcttcctaca ccgctatatc gggtgccagc 600  
 cttgtgaata ttcttgattt taaactggca aaagggtgtag gcgactacat agcaagatgt 660  
 caaacttatg aagggtggtat tgctggggag ccttatgctg aagcacatgg tgggtataca 720

ttctgtggat tggctgcttt gatcctgctt aatgaggcag agaaagttga cttgcctagt 780  
 ttgattggct gggtggcttt tcgtcaagga gtggaatgcg gatttcaagg acgaactaat 840  
 aaatttggtg atggttgcta ctccttttgg cagggagctg ccattgcttt cacacaaaag 900  
 ttaattacga ttgttgataa gcaattgaag tcctcgatt cctgcaaaaag gccatcagga 960  
 gaggatgcct gcagcaccag ttcatatggg tgcaccgcga aaaagtcttc ctctgctgtg 1020  
 gactatgcga agtttggatt tgattttata caacagagca accaaattgg cccactcttc 1080  
 cataacattg ccctgcaaca atacatccta ctttgttctc aggtactaga gggaggcttg 1140  
 agggataagc ctggaaagaa cagagatcac tatcattcat gctactgcct cagtggcctc 1200  
 gcagttagcc agtacagtgc catgactgat actggttcgt gccattacc tcagcatgtg 1260  
 cttggaccgt actctaattt gctggagcca atccatccac tctacaatgt tgtcctagat 1320  
 aagtaccata cagcctatga gttcttctca gaagagtga 1359

<210> 12  
 <211> 452  
 <212> PRT  
 <213> Zea mays

<400> 12

Met Asp Pro Ser Pro Gln Ser Thr Pro Pro Thr Gly Asp Asp Pro Ala  
 1 5 10 15

Ala Ala Ala Asp Pro Asp Leu Pro Arg Leu Thr Val Thr Gln Val Glu  
 20 25 30

Gln Met Lys Val Glu Ala Arg Val Gly Asp Ile Tyr Arg Ser Leu Phe  
 35 40 45

Gly Ala Ala Pro Asn Thr Lys Ser Ile Met Leu Glu Leu Trp Arg Asp  
 50 55 60

Gln His Ile Glu Tyr Leu Thr Pro Gly Leu Arg His Met Gly Pro Ala  
 65 70 75 80

Phe His Val Leu Asp Ala Asn Arg Pro Trp Leu Cys Tyr Trp Met Val  
 85 90 95

His Pro Leu Ala Leu Leu Asp Glu Ala Leu Asp Asp Asp Leu Glu Asn  
 100 105 110

Asp Ile Ile Asp Phe Leu Ala Arg Cys Gln Asp Lys Asp Gly Gly Tyr  
 115 120 125

Ser Gly Gly Pro Gly Gln Leu Pro His Leu Ala Thr Thr Tyr Ala Ala  
 130 135 140

Val Asn Thr Leu Val Thr Ile Gly Ser Glu Arg Ala Leu Ser Ser Ile  
 145 150 155 160

Asn Arg Gly Asn Leu Tyr Asn Phe Met Leu Gln Met Lys Asp Val Ser  
 165 170 175

Gly Ala Phe Arg Met His Asp Gly Gly Glu Ile Asp Val Arg Ala Ser  
 180 185 190

Tyr Thr Ala Ile Ser Val Ala Ser Leu Val Asn Ile Leu Asp Phe Lys  
 195 200 205

Leu Ala Lys Gly Val Gly Asp Tyr Ile Ala Arg Cys Gln Thr Tyr Glu  
 210 215 220

Gly Gly Ile Ala Gly Glu Pro Tyr Ala Glu Ala His Gly Gly Tyr Thr  
 225 230 235 240  
 Phe Cys Gly Leu Ala Ala Leu Ile Leu Leu Asn Glu Ala Glu Lys Val  
 245 250 255  
 Asp Leu Pro Ser Leu Ile Gly Trp Val Ala Phe Arg Gln Gly Val Glu  
 260 265 270  
 Cys Gly Phe Gln Gly Arg Thr Asn Lys Leu Val Asp Gly Cys Tyr Ser  
 275 280 285  
 Phe Trp Gln Gly Ala Ala Ile Ala Phe Thr Gln Lys Leu Ile Thr Ile  
 290 295 300  
 Val Asp Lys Gln Leu Lys Ser Ser Tyr Ser Cys Lys Arg Pro Ser Gly  
 305 310 315 320  
 Glu Asp Ala Cys Ser Thr Ser Ser Tyr Gly Cys Thr Ala Lys Lys Ser  
 325 330 335  
 Ser Ser Ala Val Asp Tyr Ala Lys Phe Gly Phe Asp Phe Ile Gln Gln  
 340 345 350  
 Ser Asn Gln Ile Gly Pro Leu Phe His Asn Ile Ala Leu Gln Gln Tyr  
 355 360 365  
 Ile Leu Leu Cys Ser Gln Val Leu Glu Gly Gly Leu Arg Asp Lys Pro  
 370 375 380  
 Gly Lys Asn Arg Asp His Tyr His Ser Cys Tyr Cys Leu Ser Gly Leu  
 385 390 395 400  
 Ala Val Ser Gln Tyr Ser Ala Met Thr Asp Thr Gly Ser Cys Pro Leu  
 405 410 415  
 Pro Gln His Val Leu Gly Pro Tyr Ser Asn Leu Leu Glu Pro Ile His  
 420 425 430  
 Pro Leu Tyr Asn Val Val Leu Asp Lys Tyr His Thr Ala Tyr Glu Phe  
 435 440 445  
 Phe Ser Glu Glu  
 450

<210> 13  
 <211> 1031  
 <212> DNA  
 <213> *Oryza sativa*

<400> 13  
 gcacgagggc gtagccgcct ttcggtgaga tccccgcggc tgcagcgagc tgcgaggccg 60  
 ccgccttccg cgccgccgac caccgcgccc atggaccccc cctcgccgcc gccgccgccg 120  
 ccatactctc ctgctgctgc tgagggcggt ccggcagcgg atagccaggc cgctgagctg 180  
 ccccggtga ctgtgacgca ggtggagcag atgaaggtgg aggcgaaggt gggcgaaatc 240  
 taccgcgtcc tcttcggcaa cgcgcccaac gccaatccc tcatgttaga gctgtggcgt 300  
 gagcagcatg ttgagtattt gacgagaggg ctgaaacatc ttggaccaag cttccatgtg 360  
 ctcgatgcc aatcgacctg gctgtgctac tggattattc atgcacttgc tctgttggat 420  
 gaaataacctg acgatgttga ggatgatatt gtggacttct tatctcgatg tcaggacaaa 480  
 gatggtggtt atggcgaggg acctggacag ttgcctcatc tcgctacaac ttatgtctgt 540

gtaaatacac ttgtaactat agggagtgaag agggcactat catcggtaaa cagggacaac 600  
 ctgtacaagt tcatgcttcg gatgaaagat acatcgggag ctttcagaat gcatgatggt 660  
 ggtgaaatag atgttcgtgc tagctatact gcaatatcgg ttgccagcct tgtgaacatt 720  
 cttgatggtg aactagcaaa aggtgttgga aattacataa caaggtgtca aacctatgaa 780  
 ggtggcattg ctggggaacc gtatgctgaa gctcatggtg ggtacacttt ttgtgggctg 840  
 gctacgatga tcctgcttaa cgaagtggac aaacttgatt tggctagctt gattggctgg 900  
 gtggcatttc gccaaaggag ggaatgtgga tttcaaggac gaactaataa attggttgat 960  
 ggttgctact ccttttggca gggagctgct cttgctttta ctgttcaccg cgtggcgccg 1020  
 actgccaaac g 1031

<210> 14  
 <211> 313  
 <212> PRT  
 <213> *Oryza sativa*

<400> 14

Met Asp Pro Pro Ser Pro Pro Pro Pro Pro Tyr Pro Pro Ala Ala  
 1 5 10 15

Ala Glu Gly Gly Pro Ala Ala Asp Ser Gln Ala Ala Glu Leu Pro Arg  
 20 25 30

Leu Thr Val Thr Gln Val Glu Gln Met Lys Val Glu Ala Lys Val Gly  
 35 40 45

Glu Ile Tyr Arg Val Leu Phe Gly Asn Ala Pro Asn Ala Asn Ser Leu  
 50 55 60

Met Leu Glu Leu Trp Arg Glu Gln His Val Glu Tyr Leu Thr Arg Gly  
 65 70 75 80

Leu Lys His Leu Gly Pro Ser Phe His Val Leu Asp Ala Asn Arg Pro  
 85 90 95

Trp Leu Cys Tyr Trp Ile Ile His Ala Leu Ala Leu Leu Asp Glu Ile  
 100 105 110

Pro Asp Asp Val Glu Asp Asp Ile Val Asp Phe Leu Ser Arg Cys Gln  
 115 120 125

Asp Lys Asp Gly Gly Tyr Gly Gly Gly Pro Gly Gln Leu Pro His Leu  
 130 135 140

Ala Thr Thr Tyr Ala Ala Val Asn Thr Leu Val Thr Ile Gly Ser Glu  
 145 150 155 160

Arg Ala Leu Ser Ser Val Asn Arg Asp Asn Leu Tyr Lys Phe Met Leu  
 165 170 175

Arg Met Lys Asp Thr Ser Gly Ala Phe Arg Met His Asp Gly Gly Glu  
 180 185 190

Ile Asp Val Arg Ala Ser Tyr Thr Ala Ile Ser Val Ala Ser Leu Val  
 195 200 205

Asn Ile Leu Asp Gly Glu Leu Ala Lys Gly Val Gly Asn Tyr Ile Thr  
 210 215 220

Arg Cys Gln Thr Tyr Glu Gly Gly Ile Ala Gly Glu Pro Tyr Ala Glu  
 225 230 235 240

Ala His Gly Gly Tyr Thr Phe Cys Gly Leu Ala Thr Met Ile Leu Leu  
245 250 255

Asn Glu Val Asp Lys Leu Asp Leu Ala Ser Leu Ile Gly Trp Val Ala  
260 265 270

Phe Arg Gln Gly Val Glu Cys Gly Phe Gln Gly Arg Thr Asn Lys Leu  
275 280 285

Val Asp Gly Cys Tyr Ser Phe Trp Gln Gly Ala Ala Leu Ala Leu Thr  
290 295 300

Val His Arg Val Ala Pro Thr Ala Lys  
305 310

<210> 15  
<211> 1504  
<212> DNA  
<213> Glycine max

<400> 15  
gcacgaggac aaatccgccg ccgccgccgc cgtgtccgac ggtgagtcaa cgtgagcaat 60  
ggatggtaga gtcgcagggtg ttccagattt accaactctt cgccaccatt cctcgcaacg 120  
cccaaaccct catgttggag ctccaacgcg ataatacat gcagtatgtc tccaaaggcc 180  
ttcgccatct cagttccgca ttttccgttt tggacgctaa tcgaccctgg ctctgctact 240  
ggatcttcca ctccattgct ttgtcgggag aatccgtcga tgatgaactc gaagataacg 300  
ctatcgattt tcttaaccgt tgccaggatc cgaatgggtg atatgccggg ggaccaggcc 360  
agatgcctca tattgccaca acttatgctg ctgttaattc acttattact ttgggtggtg 420  
agaaatccct ggcatcaatt aatagagata aactgtatgg gtttctgcgg cggatgaagc 480  
aaccaaatgg tggattcagg atgcatgatg aaggtgaaat tgatgttcga gcttgctaca 540  
ctgccatttc tgttgcaagt gttttgaaca ttttggatga tgagctgatc cagaatgttg 600  
gagactacat tataagctgt caaacatatg aggggtggcat tgctgggtgag cctgggttctg 660  
aggctcatgg tgggtacacc ttttgtggat tagctacaat gattctgatt ggtgaggtta 720  
atcaacttga tctgcctcga ttagttgact ggggtggtatt ccgacaaggt aaggaatgtg 780  
gattccaggg gagaacaaat aaactggtgg atggatgcta ttccttttgg caggagggtg 840  
ctggttgctct attgcaaaga ttatcttcta ttatcaacaa acagatggaa gagacatcac 900  
agatttttgc ggtatcttat gtatctgaag caaaagaaag tttggatgga acctctagtc 960  
atgcaacatg ccgtgggtgag catgaaggca ccagtgaatc cagttcatct gattttaaaa 1020  
atattgccta taaattttatt aatgagtggg gagcacaaga accacttttt cacagtattg 1080  
ctttacagca atatattctc ttatgtgcac aggagcaaga ggggtggactg agagacaaac 1140  
cgggtaaacg tagagatcat tatcacacat gttactgttt aagtggactc tcattgtgcc 1200  
agtatagtgt gtcaaagcac ccagattctc caccactgcc taatctagta ttaggccctt 1260  
actctaactc cttagaacca atccaccccc tctttaatgt tgtcttggga cgatatcgtg 1320  
aagctcatga attcttcttt actgagtcgt gaccactggt tttagctacc aacaacttta 1380  
tttgataaat gtaaaataaa ttcattggaa catataaatg taaaacagca ttggattaaa 1440  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaa 1504

<210> 16  
<211> 429  
<212> PRT  
<213> Glycine max

<400> 16  
Met Val Glu Ser Gln Val Phe Gln Ile Tyr Gln Leu Phe Ala Thr Ile  
1 5 10 15

Pro Arg Asn Ala Gln Thr Leu Met Leu Glu Gln Arg Asp Asn His  
20 25 30

Met	Gln	Tyr	Val	Ser	Lys	Gly	Leu	Arg	His	Leu	Ser	Ser	Ala	Phe	Ser	35	40	45	
Val	Leu	Asp	Ala	Asn	Arg	Pro	Trp	Leu	Cys	Tyr	Trp	Ile	Phe	His	Ser	50	55	60	
Ile	Ala	Leu	Ser	Gly	Glu	Ser	Val	Asp	Asp	Glu	Leu	Glu	Asp	Asn	Ala	65	70	75	80
Ile	Asp	Phe	Leu	Asn	Arg	Cys	Gln	Asp	Pro	Asn	Gly	Gly	Tyr	Ala	Gly	85	90	95	
Gly	Pro	Gly	Gln	Met	Pro	His	Ile	Ala	Thr	Thr	Tyr	Ala	Ala	Val	Asn	100	105	110	
Ser	Leu	Ile	Thr	Leu	Gly	Gly	Glu	Lys	Ser	Leu	Ala	Ser	Ile	Asn	Arg	115	120	125	
Asp	Lys	Leu	Tyr	Gly	Phe	Leu	Arg	Arg	Met	Lys	Gln	Pro	Asn	Gly	Gly	130	135	140	
Phe	Arg	Met	His	Asp	Glu	Gly	Glu	Ile	Asp	Val	Arg	Ala	Cys	Tyr	Thr	145	150	155	160
Ala	Ile	Ser	Val	Ala	Ser	Val	Leu	Asn	Ile	Leu	Asp	Asp	Glu	Leu	Ile	165	170	175	
Gln	Asn	Val	Gly	Asp	Tyr	Ile	Ile	Ser	Cys	Gln	Thr	Tyr	Glu	Gly	Gly	180	185	190	
Ile	Ala	Gly	Glu	Pro	Gly	Ser	Glu	Ala	His	Gly	Gly	Tyr	Thr	Phe	Cys	195	200	205	
Gly	Leu	Ala	Thr	Met	Ile	Leu	Ile	Gly	Glu	Val	Asn	His	Leu	Asp	Leu	210	215	220	
Pro	Arg	Leu	Val	Asp	Trp	Val	Val	Phe	Arg	Gln	Gly	Lys	Glu	Cys	Gly	225	230	235	240
Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu	Val	Asp	Gly	Cys	Tyr	Ser	Phe	Trp	245	250	255	
Gln	Gly	Gly	Ala	Val	Ala	Leu	Leu	Gln	Arg	Leu	Ser	Ser	Ile	Ile	Asn	260	265	270	
Lys	Gln	Met	Glu	Glu	Thr	Ser	Gln	Ile	Phe	Ala	Val	Ser	Tyr	Val	Ser	275	280	285	
Glu	Ala	Lys	Glu	Ser	Leu	Asp	Gly	Thr	Ser	Ser	His	Ala	Thr	Cys	Arg	290	295	300	
Gly	Glu	His	Glu	Gly	Thr	Ser	Glu	Ser	Ser	Ser	Ser	Asp	Phe	Lys	Asn	305	310	315	320
Ile	Ala	Tyr	Lys	Phe	Ile	Asn	Glu	Trp	Arg	Ala	Gln	Glu	Pro	Leu	Phe	325	330	335	
His	Ser	Ile	Ala	Leu	Gln	Gln	Tyr	Ile	Leu	Leu	Cys	Ala	Gln	Glu	Gln	340	345	350	

Glu Gly Gly Leu Arg Asp Lys Pro Gly Lys Arg Arg Asp His Tyr His  
355 360 365

Thr Cys Tyr Cys Leu Ser Gly Leu Ser Leu Cys Gln Tyr Ser Trp Ser  
370 375 380

Lys His Pro Asp Ser Pro Pro Leu Pro Asn Leu Val Leu Gly Pro Tyr  
385 390 395 400

Ser Asn Leu Leu Glu Pro Ile His Pro Leu Phe Asn Val Val Leu Gly  
405 410 415

Arg Tyr Arg Glu Ala His Glu Phe Phe Phe Thr Glu Ser  
420 425

<210> 17  
<211> 533  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (499)

<220>  
<221> unsure  
<222> (525)

<400> 17  
gagagagata cgaatccggc ggccggcgcca ccgtgtccga cggtgagtca acgggaccag 60  
tggatggtag agtcgcaggt gtttcagatt taccaactct ttgccaccat tcctggcagc 120  
gccccaaaacc tcatgttaga gctgcaacgc gataatcaca tgcagtatct ctccaaaggc 180  
ctacgccatc tcagttccgc gttttctgtc ttggacgcta atcgaccctg gctctgttac 240  
tggatcttcc attccattgc tttgctggga gaatccgtcg acgacgaact cgaagataac 300  
actatcgatt ttcttaaccg ttgccaggat ccgaatggtg gatatgctgg gggaccaggc 360  
cagatgcctc acattgccac aacatatgct gcagttaata cacttattac tttgggtggt 420  
cagaaatcct ggcataatt aataggtgag ataaactgta tgggtttctg cggcgatga 480  
agcaatcaaa tggggggant caagatgcat gatgaaagga gaaanttgat gtc 533

<210> 18  
<211> 141  
<212> PRT  
<213> Glycine max

<400> 18  
Asp Thr Asn Pro Ala Ala Ala Pro Pro Cys Pro Thr Val Ser Gln Arg  
1 5 10 15

Asp Gln Trp Met Val Glu Ser Gln Val Phe Gln Ile Tyr Gln Leu Phe  
20 25 30

Ala Thr Ile Pro Gly Ser Ala Gln Asn Leu Met Leu Glu Leu Gln Arg  
35 40 45

Asp Asn His Met Gln Tyr Leu Ser Lys Gly Leu Arg His Leu Ser Ser  
50 55 60

Ala Phe Ser Val Leu Asp Ala Asn Arg Pro Trp Leu Cys Tyr Trp Ile  
65 70 75 80

Phe His Ser Ile Ala Leu Leu Gly Glu Ser Val Asp Asp Glu Leu Glu  
85 90 95

Asp Asn Thr Ile Asp Phe Leu Asn Arg Cys Gln Asp Pro Asn Gly Gly  
100 105 110

Tyr Ala Gly Gly Pro Gly Gln Met Pro His Ile Ala Thr Thr Tyr Ala  
115 120 125

Ala Val Asn Thr Leu Ile Thr Leu Gly Gly Gln Lys Ser  
130 135 140

<210> 19

<211> 333

<212> PRT

<213> Pisum sativum

<400> 19

Met Ala Gly Asn Ile Glu Val Glu Glu Asp Asp Arg Val Pro Leu Arg  
1 5 10 15

Leu Arg Pro Glu Trp Ser Asp Val Thr Pro Ile Pro Gln Asp Asp Gly  
20 25 30

Pro Ser Pro Val Val Pro Ile Asn Tyr Ser Glu Glu Phe Ser Glu Val  
35 40 45

Met Asp Tyr Phe Arg Ala Val Tyr Phe Ala Lys Glu Leu Ser Ser Arg  
50 55 60

Ala Leu Ala Leu Thr Ala Glu Ala Ile Gly Leu Asn Ala Gly Asn Tyr  
65 70 75 80

Thr Val Trp His Phe Arg Arg Leu Leu Leu Glu Ser Leu Lys Val Asp  
85 90 95

Leu His Val Glu Arg Glu Phe Val Glu Arg Val Ala Ser Gly Asn Ser  
100 105 110

Lys Asn Tyr Gln Ile Trp His His Arg Arg Trp Val Ala Glu Lys Leu  
115 120 125

Gly Pro Glu Ala Arg Asn Ser Glu Leu Glu Phe Thr Lys Lys Ile Leu  
130 135 140

Ser Val Asp Ala Lys His Tyr His Ala Trp Ser His Arg Gln Trp Val  
145 150 155 160

Leu Gln Asn Leu Gly Gly Trp Glu Asp Glu Leu Ser Tyr Cys Ser Glu  
165 170 175

Leu Leu Ala Glu Asp Ile Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr  
180 185 190

Phe Val Ile Thr Arg Ser Pro Val Leu Gly Gly Leu Lys Ala Met Arg  
195 200 205

Glu Ser Glu Val Leu Phe Thr Val Glu Ala Ile Ile Ser Tyr Pro Glu  
210 215 220



Asn Glu Ser Ser Trp Arg Tyr Leu Arg Gly Leu Phe Lys Asp Glu Ser  
 225 230 235 240  
 Thr Leu Tyr Val Asn Asp Ala Gln Val Ser Ser Leu Cys Leu Lys Ile  
 245 250 255  
 Leu Lys Thr Lys Ser Asn Tyr Leu Phe Ala Leu Ser Thr Leu Leu Asp  
 260 265 270  
 Leu Ser Ala Ser Val Ile Gln Pro Asn Glu Asp Phe Arg Asp Ala Ile  
 275 280 285  
 Glu Ala Leu Arg Leu Gln Ile Leu Ile Lys Gln Asp Ser Asp Ile Ala  
 290 295 300  
 Ile Thr Ile Cys Ser Ile Leu Glu Gln Val Asp Pro Ile Arg Val Asn  
 305 310 315 320  
 Tyr Trp Val Trp Arg Lys Ser Arg Leu Pro Gln Ala Ala  
 325 330

<210> 20  
 <211> 326  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 20  
 Met Asn Phe Asp Glu Thr Val Pro Leu Ser Gln Arg Leu Glu Trp Ser  
 1 5 10 15  
 Asp Val Val Pro Leu Thr Gln Asp Asp Gly Pro Asn Pro Val Val Pro  
 20 25 30  
 Ile Ala Tyr Lys Glu Glu Phe Arg Glu Thr Met Asp Tyr Phe Arg Ala  
 35 40 45  
 Ile Tyr Phe Ser Asp Glu Arg Ser Pro Arg Ala Leu Arg Leu Thr Glu  
 50 55 60  
 Glu Thr Leu Leu Leu Asn Ser Gly Asn Tyr Thr Val Trp His Phe Arg  
 65 70 75 80  
 Arg Leu Val Leu Glu Ala Leu Asn His Asp Leu Phe Glu Glu Leu Glu  
 85 90 95  
 Phe Ile Glu Arg Ile Ala Glu Asp Asn Ser Lys Asn Tyr Gln Leu Trp  
 100 105 110  
 His His Arg Arg Trp Val Ala Glu Lys Leu Gly Pro Asp Val Ala Gly  
 115 120 125  
 Arg Glu Leu Glu Phe Thr Arg Arg Val Leu Ser Leu Asp Ala Lys His  
 130 135 140  
 Tyr His Ala Trp Ser His Arg Gln Trp Thr Leu Arg Ala Leu Gly Gly  
 145 150 155 160  
 Trp Glu Asp Glu Leu Asp Tyr Cys His Glu Leu Leu Glu Ala Asp Val  
 165 170 175

Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr Tyr Val Ile Thr Gln Ser  
 180 185 190  
 Pro Leu Leu Gly Gly Leu Glu Ala Met Arg Glu Ser Glu Val Ser Tyr  
 195 200 205  
 Thr Ile Lys Ala Ile Leu Thr Asn Pro Ala Asn Glu Ser Ser Trp Arg  
 210 215 220  
 Tyr Leu Lys Ala Leu Tyr Lys Asp Asp Lys Glu Ser Trp Ile Ser Asp  
 225 230 235 240  
 Pro Ser Val Ser Ser Val Cys Leu Asn Val Leu Ser Arg Thr Asp Cys  
 245 250 255  
 Phe His Gly Phe Ala Leu Ser Thr Leu Leu Asp Leu Leu Cys Asp Gly  
 260 265 270  
 Leu Arg Pro Thr Asn Glu His Lys Asp Ser Val Arg Ala Leu Ala Asn  
 275 280 285  
 Glu Glu Pro Glu Thr Asn Leu Ala Asn Leu Val Cys Thr Ile Leu Gly  
 290 295 300  
 Arg Val Asp Pro Ile Arg Ala Asn Tyr Trp Ala Trp Arg Lys Ser Lys  
 305 310 315 320  
 Ile Thr Val Ala Ala Ile  
 325  
 <210> 21  
 <211> 470  
 <212> PRT  
 <213> Lycopersicon esculentum  
 <400> 21  
 Met Glu Ser Arg Lys Val Thr Lys Thr Leu Glu Asp Gln Trp Val Val  
 1 5 10 15  
 Glu Arg Arg Val Arg Glu Ile Tyr Asp Tyr Phe Tyr Ser Ile Ser Pro  
 20 25 30  
 Asn Ser Pro Ser Asp Leu Ile Glu Ile Glu Arg Asp Lys His Phe Gly  
 35 40 45  
 Tyr Leu Ser Gln Gly Leu Arg Lys Leu Gly Pro Ser Phe Ser Val Leu  
 50 55 60  
 Asp Ala Ser Arg Pro Trp Leu Cys Tyr Trp Thr Leu His Ser Ile Ala  
 65 70 75 80  
 Leu Leu Gly Glu Ser Ile Gly Gly Lys Leu Glu Asn Asp Ala Ile Asp  
 85 90 95  
 Phe Leu Thr Arg Cys Gln Asp Lys Asp Gly Gly Tyr Gly Gly Gly Pro  
 100 105 110  
 Gly Gln Met Pro His Leu Ala Thr Thr Tyr Ala Ala Val Asn Ser Leu  
 115 120 125

Ile Thr Leu Gly Lys Pro Glu Ala Leu Ser Ser Ile Asn Arg Glu Lys 130 135 140
Leu Tyr Thr Phe Leu Leu Arg Met Lys Asp Ala Ser Gly Gly Phe Arg 145 150 155 160
Met His Asp Gly Gly Glu Val Asp Val Arg Ala Cys Tyr Thr Ala Ile 165 170 175
Ser Val Ala Asn Ile Leu Asn Ile Val Asp Asp Glu Leu Ile His Gly 180 185 190
Val Gly Asn Tyr Ile Leu Ser Cys Gln Thr Tyr Glu Gly Gly Ile Ala 195 200 205
Gly Glu Pro Gly Ser Glu Ala His Gly Gly Tyr Thr Phe Cys Gly Leu 210 215 220
Ala Ala Met Ile Leu Ile Asn Glu Val Asp Arg Leu Asp Leu Pro Gly 225 230 235 240
Leu Ile Asp Trp Val Val Phe Arg Gln Gly Val Glu Gly Gly Phe Gln 245 250 255
Gly Arg Thr Asn Lys Leu Val Asp Gly Cys Tyr Ser Phe Trp Gln Gly 260 265 270
Ala Val Val Phe Leu Ile Gln Arg Leu Asn Leu Ile Val His Glu Gln 275 280 285
Leu Gly Leu Ser Asn Asp Leu Ser Thr Glu Ser Ala Asp Asp Ser Ser 290 295 300
Glu Ser Glu Leu Ser Asp Glu Glu Glu His Leu Glu Gly Ile Ser Ser 305 310 315 320
His Val Gln Asp Thr Phe Pro Leu Gly Gln Ala Gly Ala Cys Gln Glu 325 330 335
Asn Ala Ser His Ser Pro Lys Ile Ala Asp Thr Gly Tyr Glu Phe Ile 340 345 350
Asn Arg Pro Ile Ala Met Arg Pro Leu Phe Asp Ser Met Tyr Leu Gln 355 360 365
Gln Tyr Val Leu Leu Cys Ser Gln Ile Glu Val Gly Gly Phe Arg Asp 370 375 380
Lys Pro Gly Lys Gly Arg Asp Tyr Tyr His Thr Cys Tyr Cys Leu Ser 385 390 395 400
Gly Leu Ser Ile Ala Gln Tyr Ser Trp Thr Asp Glu Ala Asp Ser Thr 405 410 415
Pro Leu Pro Arg Asp Val Phe Gly Pro Tyr Ser Lys Cys Leu Leu Glu 420 425 430
Gln Val His Pro Leu Phe Asn Val Val Leu Asp Arg Tyr Tyr Glu Ala 435 440 445

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35 40 45

Cys Tyr Trp Ile Ile His Ser Ile Ala Leu Leu Gly Glu Ser Ile Asp  
50 55 60

Asp Asp Leu Glu Asp Asn Thr Val Asp Phe Leu Asn Arg Cys Gln Asp  
65 70 75 80

Pro Asn Gly Gly Tyr Ala Gly Gly Pro Gly Gln Met Pro His Leu Ala  
85 90 95

Thr Thr Tyr Ala Ala Val Asn Thr Leu Ile Thr Leu Gly Gly Glu Lys  
100 105 110

Ser Leu Ala Ser Ile Asn Arg Asn Lys Leu Tyr Gly Phe Met Arg Arg  
115 120 125

Met Lys Gln Pro Asn Gly Gly Phe Arg Met His Asp Glu Gly Glu Ile  
130 135 140

Asp Val Arg Ala Cys Tyr Thr Ala Ile Ser Val Ala Ser Val Leu Asn  
145 150 155 160

Ile Leu Asp Asp Glu Leu Ile Lys Asn Val Gly Asp Phe Ile Leu Ser  
165 170 175

Cys Gln Thr Tyr Glu Gly Gly Leu Ala Gly Glu Pro Gly Ser Glu Ala  
180 185 190

His Gly Gly Tyr Thr Phe Cys Gly Leu Ala Ala Met Ile Leu Ile Gly  
195 200 205

Glu Val Asn Arg Leu Asp Leu Pro Arg Leu Leu Asp Trp Val Val Phe  
210 215 220

Arg Gln Gly Lys Glu Cys Gly Phe Gln Gly Arg Thr Asn Lys Leu Val  
225 230 235 240

Asp Gly Cys Tyr Ser Phe Trp Gln Gly Gly Ala Val Ala Leu Leu Gln  
245 250 255

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Arg Leu His Ser Ile Ile Asp Glu Gln Met Ala Glu Ala Ser Gln Phe  
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Val Thr Val Ser Asp Ala Pro Glu Glu Lys Glu Cys Leu Asp Gly Thr  
275 280 285

Ser Ser His Ala Thr Ser His Ile Arg His Glu Gly Met Asn Glu Ser  
290 295 300

Cys Ser Ser Asp Val Lys Asn Ile Gly Tyr Asn Phe Ile Ser Glu Trp  
305 310 315 320

Arg Gln Ser Glu Pro Leu Phe His Ser Ile Ala Leu Gln Gln Tyr Ile  
325 330 335

Leu Leu Cys Ser Gln Glu Gln Asp Gly Gly Leu Arg Asp Lys Pro Gly  
340 345 350

Lys Arg Arg Asp His Tyr His Ser Cys Tyr Cys Leu Ser Gly Leu Ser  
355 360 365

Leu Cys Gln Tyr Ser Trp Ser Lys Arg Pro Asp Ser Pro Pro Leu Pro  
370 375 380

Lys Val Val Met Gly Pro Tyr Ser Asn Leu Leu Glu Pro Ile His Pro  
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Ser Gln Leu

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Phe Ala Asn Ile Pro Pro Asn Ala Gln Ser Ile Ile Arg Pro Trp Leu  
35 40 45

Cys Tyr Trp Ile Ile His Ser Ile Ala Leu Leu Gly Glu Ser Ile Asp  
50 55 60

Asp Asp Leu Glu Asp Asn Thr Val Asp Phe Leu Asn Arg Cys Gln Asp  
65 70 75 80

Pro Asn Gly Gly Tyr Ala Gly Gly Pro Gly Gln Met Pro His Leu Ala  
85 90 95

Thr Thr Tyr Ala Ala Val Asn Thr Leu Ile Thr Leu Gly Gly Glu Lys  
100 105 110

**SECRET**